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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.71318 Seconds

(without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613b-19

Perfect score: 599

Sequence: 1 JMWATFOQKHIIKTPICNT.....ICVKNQYVHFAGIGRCP 110

Scoring table: BLJSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	579.5	96.7	111	1	RNPO_RANCA
2	445	74.3	111	1	LECS_RANCA
3	369.	61.6	111	1	RNPL_RANCA
4	267.5	44.7	104	1	R3J0_RANPI
5	154.5	25.8	145	1	ANG3_MOUSE
6	149.5	25.0	145	1	ANGR_MOUSE
7	136.5	22.8	145	1	ANGI_MOUSE
8	128.5	21.5	167	1	RNBR_BOVIN
9	125.5	21.0	124	1	RNP_BALAC
10	124.5	20.8	123	1	ANG2_BOVIN
11	123.5	20.6	124	1	RNP_PIG
12	123.5	20.6	151	1	RNBR_CARCA
13	123	20.5	146	1	ANGI_MIORA
14	123	20.5	146	1	ANGI_SAIOS
15	122.5	20.5	119	1	RNP_IGUIC
16	122.5	20.5	141	1	RNBR_GIRCA
17	122.5	20.5	151	1	RNBR_AXIPR
18	120	20.0	146	1	ANGI_CERAE
19	120	20.0	147	1	ANGI_PONPY
20	118.5	19.8	123	1	ANGI_PIG
21	118.5	19.8	143	1	RNBR_SHEEP
22	118	19.7	122	1	RNP_MACRU
23	118	19.7	146	1	ANGI_AOTTR
24	117.5	19.6	124	1	RNP_ANTAM
25	117	19.3	124	1	ANGI_SAGE
26	115.5	19.3	128	1	RNP_MYOCO
27	115	19.2	146	1	ANGI_MACMU
28	114	19.0	148	1	ANGI_BOVIN
29	113.5	18.9	124	1	RNP_CAMDR
30	113	18.9	147	1	ANGI_HUMAN
31	113	18.9	147	1	ANGI_PANTR
32	112.5	18.8	128	1	RNP_HORSE
33	111.5	18.6	128	1	RNP_PROGU

34	110.5	18.4	124	1	RNP_RANRA	P00666	rangifer la
35	110.5	18.4	149	1	RNP_MOUSE	P00663	mus musculus
36	109.5	18.3	124	1	RNP_CARCA	P00664	capreolus c
37	109.5	18.3	148	1	RN14_MOUSE	O913H1	mus musculus
38	109	18.2	125	1	ANGI_RABIT	P31347	oryctolagus
39	109	18.2	146	1	ANGI_PAPPA	O8W04	papio hamad
40	108.5	18.1	128	1	RNBP_CAVPO	P00679	cavia porce
41	107.5	17.9	124	1	RNP_GIRCA	P00662	giraffa cam
42	107.5	17.9	130	1	RNP_CRITO	P24717	cricketulus
43	106.5	17.8	124	1	RNP_BURBU	P00657	bubalus bub
44	106.5	17.8	148	1	RNP_PERLE	O9WU5	peromyscus
45	106.5	17.8	149	1	RNP_ACOCA	O9WU5	acomys calt

## ALIGNMENTS

RESULT 1	ID	RNPO_RANCA	STANDARD:	PRT:	111 AA.
AC	P11916:				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (static acid-binding lectin) (SBL-C).				
DE	Rana catesbeiana (bull frog).				
OC	Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
OX	NCBI_Taxid=8400;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Egg;				
RA	MEDLINE=87299649; PubMed=3304421.				
RA	Tilani K., Takio K., Kwada M., Nitta K., Sakakibara F., Kawachi H.,				
RA	Takayanagi G., Hakomori S.;				
RT	"Amino acid sequence of static acid binding lectin from frog (Rana				
RT	catesbeiana) eggs.";				
RL	Biochemistry 26:2189-2194(1987).				
RN	[2]				
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.				
RP	MEDLINE=92220613; PubMed=1373337;				
RA	Liao Y.-D.;				
RT	"A pyrimidine-quanine sequence-specific ribonuclease from Rana				
RT	catesbeiana (bullfrog) oocytes.";				
RL	Nucleic Acids Res. 20:1371-1377(1992).				
RN	[3]				
RP	CHARACTERIZATION.				
RP	TISSUE=Egg;				
RC	MEDLINE=93192604; PubMed=8448385;				
RA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawachi H.,				
RA	Takayanagi Y., Hakomori S., Tilani K.;				
RT	"Ribonuclease activity of static acid-binding lectin from Rana				
RT	catesbeiana eggs.";				
RL	Glycobiology 3:37-45(1993).				
RN	[4]				
RP	STRUCTURE BY NMR.				
RP	MEDLINE=98437383; PubMed=9761686;				
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T. H.;				
RT	"The solution structure of a cytotoxic ribonuclease from the frog				
RT	Rana catesbeiana (bullfrog).";				
RL	J. Mol. Biol. 283:231-244(1998).				
CC	-I- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE				
CC	RESIDUES WITH A 3'FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)				
CC	AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS				
CC	MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG				
CC	EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING				
CC	NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND				
CC	HUMAN ORIGIN.				
CC	-I- SUBUNIT: MONOMER.				
CC	-I- SUBCELLULAR LOCATION: Secreted.				
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PIR; A27121; A27121.				

PDB: 1BC4: 28-OCT-98.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA\_1.  
 DR ProDom: PD000535; RNaseA\_1.  
 DR SMART: SM00092; RNase\_Pc\_1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC\_1.  
 DR Hydrolase: Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 71  
 FT DISULFID 34 81  
 FT DISULFID 52 96  
 FT DISULFID 93 110  
 SQ SEQUENCE 111 AA: 12464 MW: 08C9E5F55729ECF4 CRC64;

Query Match 96.7%; Score 579.5; DB 1; Length 111;  
 Best Local Similarity 96.4%; Pred. No. 3e-56;  
 Matches 107; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 59  
 DB 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 60  
 QY 60 LSTRFOLNCTRTSIPRCPYSSRTETNYICVCKENQPVHFGIGRC 110  
 DB 61 LSTRFOLNCTRTSIPRCPYSSRTETNYICVCKENQPVHFGIGRC 111

RESULT 2  
 LECs\_RANJA STANDARD: PRT: 111 AA.  
 ID LECs\_RANJA  
 AC P18839;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sialic acid-binding lectin (EC 3.1.27.-).  
 OS Rana japonica (Japanese redbellied frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 NCBI\_TaxID=8402;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE-Egg;  
 RX MEDLINE=91035319; PubMed=2229005;  
 RA Kamiya T., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,  
 RA Takayanagi Y., Tlcanl K.;  
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)  
 RT eggs.";  
 RT J. Biochem. 108:139-143(1990).  
 RL J. Biochem. 108:139-143(1990).  
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE  
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN  
 CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS, BUT IT  
 CC DOES NOT AGGLUTININATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC PIR: JX0120; JX0120.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA\_1.  
 DR ProDom: PD000535; RNaseA\_1.  
 DR SMART: SM00092; RNase\_Pc\_1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC\_1.  
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 97 97

FT DISULFID 94 111  
 SQ SEQUENCE 111 AA: 12326 MW: FDEBDF3834ED679 CRC64;

Query Match 74.3%; Score 445; DB 1; Length 111;  
 Best Local Similarity 76.6%; Pred. No. 1.2e-41;  
 Matches 85; Conservative 8; Mismatches 16; Indels 2; Gaps 2;

QY 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 58  
 DB 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 60  
 QY 59 VLSSTRFOLNCTRTSIPRCPYSSRTETNYICVCKENQPVHFGIGRC 109  
 DB 61 VLSSTRFOLNCTRTSIPRCPYSSRTETNYICVCKENQPVHFGIGRC 111

RESULT 3  
 RNPL\_RANJA STANDARD: PRT: 111 AA.  
 ID RNPL\_RANJA  
 AC P14626;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, liver (EC 3.1.27.5).  
 OS Rana catesbeiana (Bull. frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Liver;  
 RX MEDLINE=90130374; PubMed=2613682;  
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
 RA Okazaki T., Ohgi K., Irie M.;  
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)  
 RT liver.";  
 RT J. Biochem. 106:729-735(1989).  
 RL J. Biochem. 106:729-735(1989).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC PIR: JX0085; JX0085.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA\_1.  
 DR ProDom: PD000535; RNaseA\_1.  
 DR SMART: SM00092; RNase\_Pc\_1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC\_1.  
 KW Hydrolyase; Nuclease; Endonuclease.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 104 104  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97  
 FT DISULFID 94 111  
 SQ SEQUENCE 111 AA: 12461 MW: D64BA72456C10788 CRC64;

Query Match 61.6%; Score 369; DB 1; Length 111;  
 Best Local Similarity 64.9%; Pred. No. 2.2e-33;  
 Matches 72; Conservative 9; Mismatches 28; Indels 2; Gaps 2;

QY 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 58  
 DB 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 60  
 QY 59 VLSSTRFOLNCTRTSIPRCPYSSRTETNYICVCKENQPVHFGIGRC 109  
 DB 61 VLSSTRFOLNCTRTSIPRCPYSSRTETNYICVCKENQPVHFGIGRC 111

ID	RN30_RANPI	STANDARD	PRT	104 AA.
AC	P22069			
DT	01-AUG-1991 (rel. 19, Created)			
DT	01-FEB-1994 (rel. 28, Last sequence update)			
DT	01-FEB-1995 (rel. 31, Last annotation update)			
DE	P-30 protein (EC 3.11.27.-) (Oocinase).			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoloidea; Ranidae; Rana.			
OX	NCBI_TaxId=8404;			
RN	RN (1)			
RP	SEQUENCE.			
RC	TISSUE=Embryo;			
RX	MEDLINE=91091131; Pubmed=1985866;			
RA	Ardelt W., Mikulski S.M., Shogen K.;			
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens			
RT	oocytes and early embryos. Homology to pancreatic ribonucleases."			
RL	J. Biol. Chem. 266:245-251(1991).			
RN	RN (2)			
RP	3D-STRUCTURE MODELING.			
RX	MEDLINE=93066156; Pubmed=1438177;			
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,			
RA	James M.N.G.;			
RT	"Comparative molecular modeling and crystallization of P-30 protein:			
RT	a novel antitumor protein of Rana pipiens oocytes and early			
RL	embryos."			
RN	RN (3)			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RX	MEDLINE=94160079; Pubmed=8120892;			
RA	Mosimann S.C., Ardelt W., James M.N.G.;			
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an			
RT	amphibian ribonuclease with antitumor activity."			
RL	J. Mol. Biol. 236:1141-1153(1994).			
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY			
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR			
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH			
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.			
CC	-1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PDB: 1ONC, 31-JAN-94.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00093; RNase_PC; 1.			
DR	PROSITE: PS00127; RNASE PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; 3d-structure.			
FT	MOD_RES	1	1	
FT	ACT_SITE	10	10	
FT	ACT_SITE	31	31	
FT	ACT_SITE	97	97	
FT	DISULFID	19	68	
FT	DISULFID	30	75	
FT	DISULFID	48	90	
FT	DISULFID	37	104	
FT	HELIX	3	10	
FT	STRAND	11	12	
FT	HELIX	19	22	
FT	TURN	23	24	
FT	TURN	26	30	
FT	STRAND	33	38	
FT	HELIX	41	48	
FT	TURN	49	50	
FT	STRAND	55	58	
FT	TURN	63	70	
FT	TURN	74	75	
FT	STRAND	77	84	
FT	STRAND	86	91	
FT	TURN	92	93	
FT	STRAND	94	101	
SEQ	SEQUENCE	104 AA:	11845 MW:	22A753C2P9E56664 CRC64;

[illegible]

Query Match 25.8%; Score 154.5; DB 1; Length 145;  
 Best Local Similarity 43.6%; Pred. No. 6e-10;  
 Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;

QY 33 CKRNVFTTISATVKAIC-----TCVILNLVLTSTRFQNLCTRTSITPR-PCPYSSR 85  
 DB 63 CKRVNFTHTKNNIKAIKCGKSGPYRNLR-I-SKSHFYVTTCTHKGSRPPRCQYNMF 120  
 86 TETNYICVCKENQYPVHF 103  
 121 KDERIVYIACEDGMPVHF 138

Db 121 KDERIVYIACEDGMPVHF 138

RESULT 6  
 ANGR\_MOUSE STANDARD; PRT; 145 AA.

AC 064438:  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT -01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Angiogenin-related protein precursor.  
 GN ANGRP.  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129; TISSUE=Liver.  
 RX MEDLINE=96079109; PubMed=8530072;  
 RA Brown W.E., Noble V., Subramanian V., Shapiro R.;  
 RT "The mouse angiogenin gene family: structures of an angiogenin-related  
 RL protein gene and two pseudogenes";  
 RL Genomics 29:200-206(1995).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: U22519; AAA91367.1;  
 DR HSSP: P03950; 144Y.  
 DR MGD: MGI:104984; Angp.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_Pc; 1.  
 KW Signal: Hydrophobic; Nuclease; PANCREATIC; 1.  
 FT SIGNAL 1 24  
 FT CHAIN 25 145  
 FT MOD\_RES 25 25  
 FT ACT\_SITE 37 37  
 FT ACT\_SITE 64 64  
 FT ACT\_SITE 137 137  
 FT DISULFID 50 104  
 FT DISULFID 63 115  
 FT DISULFID 81 130  
 FT SEQUENCE 145 AA; 16612 MW; 29A6EB81429CAD CRC64;

Query Match 25.0%; Score 149.5; DB 1; Length 145;  
 Best Local Similarity 44.2%; Pred. No. 2.1e-09;  
 Matches 34; Conservative 9; Mismatches 27; Indels 7; Gaps 3;

QY 33 CKRNVFTTISATVKAIC-----INLVNLTSTRFQNLCTRTSITPR-PCPYSSR 86  
 DB 63 CKRVNFTHTKNNIKAIKCGKSGPYRNLR-I-SKSHFYVTTCTHKGSRPPRCQYNMF 121

QY 87 ETNYICVCKENQYPVHF 103  
 DB 122 GFRYIIICGNGMPVHF 138

Db 122 GFRYIIICGNGMPVHF 138

RESULT 7  
 ANGI\_MOUSE STANDARD; PRT; 145 AA.

AC P21570:  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-).  
 GN ANG.  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=91025023; PubMed=2222458;  
 RA Bond M.D., Vallee B.L.;  
 RT "Isolation and sequencing of mouse angiogenin DNA";  
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Serum;  
 RX MEDLINE=93192291; PubMed=8448182;  
 RA Bond M.D., Strydom D.J., Vallee B.L.;  
 RT "Characterization and sequencing of rabbit, pig and mouse  
 RT angiogenins: discernment of functionally important residues and  
 RL regions";  
 RL Blochim. Biophys. Acta 1162:177-186(1993).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS: ONCE BOUND,  
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U22516; AAA91366.1;  
 DR PIR: A35932; A35932.  
 DR HSSP: P03950; 144Y.  
 DR MGD: MGI:88022; Ang.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_Pc; 1.  
 KW Hydroxylase; Nuclease; Endonuclease; Angiogenesis;  
 KW protein synthesis inhibitor; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 145  
 FT MOD\_RES 25 25  
 FT ACT\_SITE 37 37  
 FT ACT\_SITE 64 64  
 FT ACT\_SITE 137 137  
 FT DISULFID 50 104  
 FT DISULFID 63 115



FT DISULFID 26 84 BY SIMILARITY.  
 FT DISULFID 40 95 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 65 72 BY SIMILARITY.  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT ACT\_SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) IN 30% OF THE  
 MOLECULES.  
 SO SEQUENCE 124 AA; 14125 MW; F57475459F67E20 CRC64;

Query Match 21.0%; Score 125.5; DB 1; Length 124;  
 Best Local Similarity 31.6%; Pred. No. 7.2e-07;  
 Matches 37; Conservative 17; Mismatches 40; Indels 23; Gaps 7;

OY 6 FQOKHIT-----KTPICITLIDNNIYIGGCKRVNTTSSATTVAICTGVNLNV 59  
 DB 8 FQOKHIDGNSPPNNRYCNQMMRR-KMTGCKCKPVNFVHSLDYKAVCS---QKNV 63  
 OY 60 L-----STTRQLNTCTRTSITPR-PCYSSRTETNYICVCE-NOY-PVHF 103  
 DB 64 LCKNGRTNCEYNSTWHTDCCROTGSCKYPNCATKSQEKHIVACEGNPIYPVHF 120

RESULT 10  
 ANG2\_BOVIN  
 ID ANG2\_BOVIN STANDARD; PRT; 123 AA.  
 AC P80929;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin-2 (EC 3.1.27.-).

GN ANG2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE.

RC TISSUE-Serum, and Milk;  
 RX MEDLINE=97409980; PubMed=9266695;

RA Strydom D.J., Bond M.D., Vallee B.L.;

RT "An angiogenic protein from bovine serum and milk -- purification and  
 primary structure of angiogenin-2.";

RL Eur. J. Biochem. 247:535-544(1997).

CC - FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND  
 PRIMARY STRUCTURE OF ANGIOGENIN-2.

CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC  
 ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 HYDROLYZING CELLULAR TRNAS.

CC - TISSUE SPECIFICITY: SERUM, AND MILK.  
 CC - SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

CC HSSP: P10152; IAGI

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR ProDom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase.Pc; 1.

DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.

KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KW Protein synthesis inhibitor; Glycoprotein.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 39 39 BY SIMILARITY.  
 FT ACT\_SITE 113 113 BY SIMILARITY.  
 FT DISULFID 25 80 BY SIMILARITY.  
 FT DISULFID 38 91 BY SIMILARITY.  
 FT DISULFID 56 106 BY SIMILARITY.  
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .)

SO SEQUENCE 123 AA; 14522 MW; B703B9839919FDFE CRC64;

Query Match 20.8%; Score 124.5; DB 1; Length 123;

Best Local Similarity 29.6%; Pred. No. 9.1e-07;  
 Matches 32; Conservative 20; Mismatches 43; Indels 13; Gaps 5;

OY 6 FQOKHITPT1-----ICNTILIDNNIYIGGCKRVNTTSSATTVAICTGVNLNV 57  
 DB 8 FLKHKYPSPTGDDRCNTMMRR--NMTRPCKDNTFTHNSDDIRAVCDRNGEPPYR 65  
 OY 58 NVLSTR--FQNTCTRTSITPR-PCYSSRTETNYICVCEQNPVHF 102  
 DB 66 NGLRRSRSPQVTTCTRHGGSPRPPCYRAFRANRYIVIRCRGFPFH 113

RESULT 11

ID RNP\_PIG STANDARD; PRT; 124 AA.  
 AC P00671;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNase 1) (RNase A).

GN RNASE1 OR RN51.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE.

RX MEDLINE=70104197; PubMed=5460946;  
 RA Jackson R.L., Hirs C.H.W.;

RT "The primary structure of porcine pancreatic ribonuclease. II. The  
 amino acid sequence of the reduced S-aminoethylated protein.";

RL J. Biol. Chem. 245:637-653(1970).

RN [2]

RP REVISION TO 2.  
 RA Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;

RT "Affinity chromatography of porcine pancreatic ribonuclease and  
 reinvestigation of the N-terminal amino acid sequence.";

RL FEBS Lett. 31:181-185(1973).

RN [3]

RP DISULFIDE BONDS.

RX MEDLINE=70104198; PubMed=4904878;  
 RA Phelan J.J., Hirs C.H.W.;

RT "The primary structure of porcine pancreatic ribonuclease. 3. The  
 disulfide bonds.";

RL J. Biol. Chem. 245:654-661(1970).

CC - CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 with 2',3'-cyclic phosphate intermediates.

CC - SUBCELLULAR LOCATION: Secreted.

CC - TISSUE SPECIFICITY: PANCREAS.

CC - SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

CC PIR: A00816; NRPC.

DR HSSP: P00656; ISRN.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR ProDom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase.Pc; 1.

DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.

KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.

FT DISULFID 26 84  
 FT DISULFID 40 95  
 FT DISULFID 58 110  
 FT DISULFID 65 72  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT ACT\_SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .)  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .)  
 SO SEQUENCE 124 AA; 13804 MW; OAC28CDE14111845 CRC64;

Query Match 20.6%; Score 123.5; DB 1; Length 124;

Best Local Similarity 29.8%; Pred. No. 1.2e-06;  
Matches 34; Conservative 20; Mismatches 43; Indels 17; Gaps 6;

OY 6 F00KH1-----IKTPIICNTIILNNIYVGGCKRVNFIISATTVKATGIVINL 58  
DB 8 F0RQHIDPSSSSSSSSNPNCKNLMMSRR-NNTOGRCFVNFTFVHESLDVQAVGCSQIWNVC 66  
OY 59 VLTSTRFOLNT-----CTRTSITPRP-CPYSSRTEFTNYCVKCENO--YPVHF 103  
DB 67 NGOTNKVQSNSHTMTIDCRQTGSSKTPNCAYKASDEQKHIIYACGEPVPVPHF 120

## RESULT 12

RNRB\_CAPCA

ID RNRB\_CAPCA STANDARD: FRT; 151 AA.

AC 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
OS Capreolus capreolus (Roe deer).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;  
OC Cervidae; Odocoileinae; Capreolus.  
OX NCBI\_TaxID=9858;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98278842; PubMed=9611269;  
RA Beuvelman H.J., van der Munnik N., Kleinedam R.G., Furia A.,  
RT "Secretory ribonuclease genes and pseudogenes in true ruminants";  
RL Gene 212:259-268(1998).

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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CC EMBL: Y11673; CAA72371.1;  
CC HSP: P00656; ISRN.  
CC InterPro: IPR001427; RNaseA.  
CC Pfam: PF00074; RNaseA.1.  
CC PRINTS: PR00794; RIBONUCLEASE.  
CC ProDom: PD000535; RNaseA.1.  
CC SMART: SM00092; RNaseA\_PC.1.  
CC DR PROSITE: PS00147; RNASE\_PANCREATIC.1.  
CC KM Hydrolase; Nuclease; Endonuclease; Glycoprotein.  
CC FT ACT SITE 41 41 BY SIMILARITY.  
CC FT DISULFID 26 84 BY SIMILARITY.  
CC FT DISULFID 40 95 BY SIMILARITY.  
CC FT DISULFID 58 110 BY SIMILARITY.  
CC FT DISULFID 65 172 BY SIMILARITY.  
CC FT CARBOHYD 126 62 N-LINKED (GLCNAC...) (BY SIMILARITY).  
CC FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).  
CC FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).  
CC SQ SEQUENCE 151 AA; 16971 MW; 392D0E6302F006A6 CRC64;

Query Match 20.6%; Score 123.5; DB 1; Length 151;  
Best Local Similarity 28.6%; Pred. No. 1.5e-06;  
Matches 34; Conservative 18; Mismatches 44; Indels 23; Gaps 6;

OY 4 ATRQOQHIIK-----TPIICNTIILNNIYVGGCKRVNFIISATTVKATGIVINL 57  
DB 6 AKFRRCVHMDSGSSSSNPNCKNLMMSRR-FMTHGRCPVTFVHESLDVQAVGCSQIWNVC 61  
OY 58 NVL-----STRFOLNTCTRTSITPRP-CPYSSRTEFTNYCVKCENO--YPVHF 103  
DB 62 NITCKKQCPNCGVQSNSHTMTIDCRQTGSSKTPNCAYKASDEQKHIIYACGEPVPVPHF 120

## RESULT 13

ANGI\_MIOTA

ID ANGI\_MIOTA STANDARD: PRT; 146 AA.

AC Q8WN65;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Angiotensin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).  
GN ANG OR RNASE5.  
OS Miophilthecus talapoin (Talapoin) (Cercopithecus talapoin).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Miophilthecus.  
OX NCBI\_TaxID=36231;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiotensin in  
RT primate evolution";  
RL Mol. Biol. Evol. 19:438-445(2002).

CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS. ONCE BOUND,  
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
CC HYDROLYZING CELLULAR TRNAS (BY SIMILARITY).  
CC SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: AF041665; AML61647.1;  
CC KM Hydrolase; Nuclease; Endonuclease; Angiogenesis;  
CC KW Protein synthesis inhibitor; Signal.  
CC FT SIGNAL 1 24 BY SIMILARITY.  
CC FT CHAIN 25 146 ANGIOGENIN.  
CC FT MOD\_RES 25 25 PYROGLUTAMINE CARBOXYLIC ACID (BY  
CC SIMILARITY).  
CC FT ACT SITE 37 37 BY SIMILARITY.  
CC FT ACT SITE 64 64 BY SIMILARITY.  
CC FT ACT SITE 138 138 BY SIMILARITY.  
CC FT DISULFID 50 105 BY SIMILARITY.  
CC FT DISULFID 63 116 BY SIMILARITY.  
CC FT DISULFID 81 131 BY SIMILARITY.  
CC SQ SEQUENCE 146 AA; 16486 MW; C8C268203F5C0061 CRC64;

Query Match 20.5%; Score 123; DB 1; Length 146;  
Best Local Similarity 40.3%; Pred. No. 1.6e-06;  
Matches 31; Conservative 9; Mismatches 29; Indels 8; Gaps 3;

OY 33 CKRVNFIISATTVKATGIVINLV-----LSTTRFOLNTCTRTSITPRP-CPYSSR 85  
DB 63 CKDINFHGNRRSIAIC-GDENGPNYGENLISRPQVYTCNLRGSPRPYRYRAT 121  
OY 86 TETNYICVACENQYPVH 102  
DB 122 AGFRNIVVACENGLPVH 138  
RESULT 14  
ID ANGI\_SAISC STANDARD: PRT; 146 AA.  
AC Q8WN65;  
DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).  
GN ANG OR RNASE5.  
OS Saimiri sciureus (Common squirrel monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
OX NCBI\_TaxID=9521;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiogenin in  
RT primate evolution";  
RL Mol. Biol. Evol. 19:438-445(2002).  
CC -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
CC HYDROLYZING CELLULAR TRNAS (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: AF441670; AAL61652.1;  
DR KJ Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
KW Protein synthesis inhibitor; Signal;  
FT SIGNAL 1 24  
FT CHAIN 25 146 ANGIOGENIN.  
FT MOD\_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY  
FT ACT\_SITE 37 37 BY SIMILARITY).  
FT ACT\_SITE 64 64 BY SIMILARITY.  
FT ACT\_SITE 138 138 BY SIMILARITY.  
FT DISULFID 30 103 BY SIMILARITY.  
FT DISULFID 63 116 BY SIMILARITY.  
FT DISULFID 81 131 BY SIMILARITY.  
SQ SEQUENCE 146 AA; 16387 MW; 2E0372D0C4F7B8 CRC64;  
Query Match 20.5%; Score 123; DB 1; Length 146;  
Best Local Similarity 36.7%; Pred. No. 1.6e-06;  
Matches 29; Conservative 10; Mismatches 28; Indels 12; Gaps 3;  
QY 33 CKRVNFTFISSATVKAICTGVINL-----VLSTRPOLNCTRTSTPR-PCPYS 83  
DB 63 CKREINTIHKNSIKAIICG---NONGPYNGNORISATSQVYITICRHIGSPRPCTRY 119  
QY 84 SRTEYNYICVKNQYPVH 102  
DB 120 ATAGFRNIVIAECNGLPVH 138  
RESULT 15  
RNP\_IGUIG  
ID RNP\_IGUIG STANDARD; PRT; 119 AA.  
AC P80287;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
OS Iguana iguana (Common Iguana).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosaurs; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
OX NCBI\_TaxID=6517;

RN [1]  
RP SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=94139745; PubMed=8307028;  
RA Zhao W., Beutema J.J., Hofsteenge J.;  
RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic  
RT ribonuclease.";  
RL Eur. J. Biochem. 219:641-646(1994).  
CC -1- CATALYTIC ACTIVITY: 3'-phosphooligonucleotides ending in C-P or U-P  
CC with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: PANCREAS.  
CC -1- FUNCTION: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
CC HSSP: P00656; 1LSQ.  
DR Interpro: IPR001427; RNaseA.  
DR Pfam: PF000074; RNaseA; 1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR PRODOM: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_PC; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease.  
FT MOD\_RES 1 1 PYROLIDONE CARBOXYLIC ACID.  
FT DISULFID 25 80 BY SIMILARITY.  
FT DISULFID 39 91 BY SIMILARITY.  
FT DISULFID 57 106 BY SIMILARITY.  
FT ACT\_SITE 10 10 BY SIMILARITY.  
FT ACT\_SITE 40 40 BY SIMILARITY.  
FT ACT\_SITE 113 113 BY SIMILARITY.  
SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;  
Query Match 20.5%; Score 122.5; DB 1; Length 119;  
Best Local Similarity 29.6%; Pred. No. 1.5e-06;  
Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 5;  
QY 1 QNATFEQCKH-----IKTP-IICNTILDNNIYVGCKRVNFTFISSATVKAIC-- 51  
DB 1 QDMSSFONKHIDYPTASNPNAVCDLMQOR-NLNPCKCKTRTFVHASPSEIOVCGS 59  
QY 52 -TGVINLNLSTTRPOLNCTRTSTP-PPCPYSRTETNYICVKNQYPVHF 103  
DB 60 GGTVEEDNLVDSNPSFLTDCKNNGVGTAPSSCKTNGTPKRRIRIACENNQYPVHF 114  
Search completed: June 25, 2003, 14:50:06  
Job time : 5.71318 secs